

J. Leatherspoon

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/981,087A

NOV 14 2000

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TECH CENTER 1600/2500
INPUT SET: S33471.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

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SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Elmore, Michael J.
Mauchline, Margaret L.
Minton, Nigel P.
Pasechnik, Vladimir A.
Titball, Richard W.

(ii) TITLE OF INVENTION: TYPE F BOTULINUM TOXIN AND USE THEREOF

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: NIXON & VANDERHYE P.C.
(B) STREET: 1100 North Glebe Rd. 8th floor
(C) CITY: Arlington
(D) STATE: VA
(E) COUNTRY: USA
(F) ZIP: 22201-4741

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/981,087
(B) FILING DATE: 27-MAY-1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/GB96/01409
(B) FILING DATE: 12-JUN-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: GB 9511909.5
(B) FILING DATE: 12-JUN-1995

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Crawford, Arthur R.
(B) REGISTRATION NUMBER: 25,327
(C) REFERENCE/DOCKET NUMBER: 124-688

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47 (ix) TELECOMMUNICATION INFORMATION:
48 (A) TELEPHONE: 703-816-4000
49 (B) TELEFAX: 703-816-4100
50
51
52 (2) INFORMATION FOR SEQ ID NO:1:
53
54 (i) SEQUENCE CHARACTERISTICS:
55 (A) LENGTH: 431 amino acids
56 (B) TYPE: amino acid
57 (C) STRANDEDNESS:
58 (D) TOPOLOGY: linear
59
60 (ii) MOLECULE TYPE: peptide
61
62
63
64
65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
66
67 Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu Tyr
68 1 5 10 15
69
70 Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn Asn
71 20 25 30
72
73 Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn Gly
74 35 40 45
75
76 Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr Ser
77 50 55 60
78
79 Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile Tyr
80 65 70 75 80
81
82 Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro
83 85 90 95
84
85 Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile Asp
86 100 105 110
87
88 Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr Asn
89 115 120 125
90
91 Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys Leu
92 130 135 140
93
94 Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn Lys
95 145 150 155 160
96
97 Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg Ile
98 165 170 175
99

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100   Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu Gly
101           180                      185                      190
102
103   Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys Asn
104           195                      200                      205
105
106   Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr Glu
107           210                      215                      220
108
109   Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp Pro
110           225                      230                      235                      240
111
112   Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys Arg
113           245                      250                      255
114
115   Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln Asn
116           260                      265                      270
117
118   Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys Pro
119           275                      280                      285
120
121   Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile Ile
122           290                      295                      300
123
124   Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val Arg
125           305                      310                      315                      320
126
127   Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu Tyr
128           325                      330                      335
129
130   Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile Lys
131           340                      345                      350
132
133   Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile Val
134           355                      360                      365
135
136   Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn Asn
137           370                      375                      380
138
139   Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val Ala
140           385                      390                      395                      400
141
142   Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn Gly
143           405                      410                      415
144
145   Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn
146           420                      425                      430
147

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

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153 (C) STRANDEDNESS:
154 (D) TOPOLOGY: linear
155
156 (ii) MOLECULE TYPE: peptide
157
158
159
160
161 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
162
163 Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu Tyr
164 1 5 10 15
165
166 Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn Asn
167 20 25 30
168
169 Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn Gly
170 35 40 45
171
172 Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr Ser
173 50 55 60
174
175 Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile Tyr
176 65 70 75 80
177
178 Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro
179 85 90 95
180
181 Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile Asp
182 100 105 110
183
184 Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr Asn
185 115 120 125
186
187 Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys Leu
188 130 135 140
189
190
191 (2) INFORMATION FOR SEQ ID NO:3:
192
193 (i) SEQUENCE CHARACTERISTICS:
194 (A) LENGTH: 144 amino acids
195 (B) TYPE: amino acid
196 (C) STRANDEDNESS:
197 (D) TOPOLOGY: linear
198
199 (ii) MOLECULE TYPE: peptide
200
201
202
203
204 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
205

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206 Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn Lys
207 1 5 10 15
208
209 Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg Ile
210 20 25 30
211
212 Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu Gly
213 35 40 45
214
215 Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys Asn
216 50 55 60
217
218 Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr Glu
219 65 70 75 80
220
221 Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp Pro
222 85 90 95
223
224 Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys Arg
225 100 105 110
226
227 Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln Asn
228 115 120 125
229
230 Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys Pro
231 130 135 140
232
233

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

248 Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile Ile
249 1 5 10 15
250
251

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SEQUENCE VERIFICATION REPORT
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